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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Briskin, Michael J.
Ringler, Douglas J.
Picarella, Dominic
Newman, Walter

(ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
(B) STREET: 530 Virginia Road, PO Box 9133
(C) CITY: Concord
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 01742-9133

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/875,849
(B) FILING DATE: 08-SEP-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US96/02153
(B) FILING DATE: 12-FEB-1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/523,004
(B) FILING DATE: 01-SEP-1995

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brook, David E.
(B) REGISTRATION NUMBER: 22,592
(C) REFERENCE/DOCKET NUMBER: LKS94-04A2

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 978-341-0036
(B) TELEFAX: 978-341-0136

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC	48
Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	
CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG	96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu	
20 25 30	
CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC	144
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
35 40 45	
CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC	192
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp	
50 55 60	
ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC	240
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr	
65 70 75 80	
GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC	288
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly	
85 90 95	
TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC	336
Ser Cys Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr	
100 105 110	
GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT	384
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly	
115 120 125	
GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC	432
Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro	
130 135 140	
AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG	480
Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly	
145 150 155 160	

GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln 165 170 175	528
GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro 180 185 190	576
CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG Pro Leu Gly Thr Pro Val Pro Ala Leu Tyr Cys Gln Ala Thr Met 195 200 205	624
AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu 210 215 220	672
CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro 225 230 235 240	720
CCC AAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG TCT Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser 245 250 255	768
CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro 260 265 270	816
CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro 275 280 285	864
CCC GAC AAG ACC TCC CCG GAG CCC GCC CCC CAG CAG GGC TCC ACA CAC Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His 290 295 300	912
ACC CCC AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser 305 310 315 320	960
CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA GGC TCG TCC AAA Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys 325 330 335	1008
CCT GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val 340 345 350	1056
CTG GGA CTG CTG CTC CTG GCC TTG CCC ACG TAT CAC CTC TGG AAA CGC Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg 355 360 365	1104
TGC CGG CAC CTG GCT GAG GAC ACC CAC CCA CCA GCT TCT CTG AGG Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg 370 375 380	1152
CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln 385 390 395 400	1200

GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCCTTCCCC CTGTGAAAGC Val Gly Ile Ser Pro Ser 405	1248
AAAATAGCTT GGACCCCTTC AAGTTGAGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCT CTTTGGAGAA GCTCATCAGA AACTCAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAGGCC CTCCCTGAGT GGTCCCCACC TTTCTGGACG GAACCACGTA CTTTTACAT ACATTGATTC ATGTCTCACG TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCC CTGTCGTCAG GACCTCCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAA AAAAAAA AAAA	1308 1368 1428 1488 1548 1608 1624

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu 1 5 10 15
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu 20 25 30
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg 35 40 45
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp 50 55 60
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr 65 70 75 80
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly 85 90 95
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr 100 105 110
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly 115 120 125
Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro 130 135 140

Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
 145 150 155 160

Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
 165 170 175

Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
 180 185 190

Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
 195 200 205

Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
 210 215 220

His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
 225 230 235 240

Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
 245 250 255

Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
 260 265 270

Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
 275 280 285

Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
 290 295 300

Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
 305 310 315 320

Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
 325 330 335

Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
 340 345 350

Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
 355 360 365

Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
 370 375 380

Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
 385 390 395 400

Val Gly Ile Ser Pro Ser
 405

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC	48
Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	
CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG	96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu	
20 25 30	
CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC	144
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
35 40 45	
CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC	192
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp	
50 55 60	
ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC	240
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr	
65 70 75 80	
GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC	288
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly	
85 90 95	
TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC	336
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr	
100 105 110	
GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT	384
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly	
115 120 125	
GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC	432
Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro	
130 135 140	
AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG	480
Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly	
145 150 155 160	
GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG	528
Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln	
165 170 175	
GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG	576
Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro	
180 185 190	

CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met 195 200 205	624
AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu 210 215 220	672
CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG TCT His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Ser 225 230 235 240	720
CCC GAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CAG GAG CCT Pro Asp Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Gln Glu Pro 245 250 255	768
CCC GAC ACC ACC TCC CCG GAG CCT CCC GAC AAG ACC TCC CCG GAG CCC Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro 260 265 270	816
GCC CCC CAG CAG GGC TCC ACA CAC ACC CCC AGG AGC CCA GGC TCC ACC Ala Pro Gln Gln Gly Ser Thr His Thr Pro Arg Ser Pro Gly Ser Thr 275 280 285	864
AGG ACT CGC CGC CCT GAG ATC TCC CAG GCT GGG CCC ACG CAG GGA GAA Arg Thr Arg Arg Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu 290 295 300	912
GTG ATC CCA ACA GGC TCG TCC AAA CCT GCG GGT GAC CAG CTG CCC GCG Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala 305 310 315 320	960
GCT CTG TGG ACC AGC AGT GCG GTG CTG GGA CTG CTG CTC CTG GCC TTG Ala Leu Trp Thr Ser Ser Ala Val Leu Gly Leu Leu Leu Ala Leu 325 330 335	1008
CCC ACC TAT CAC CTC TGG AAA CGC TGC CGG CAC CTG GCT GAG GAC GAC Pro Thr Tyr His Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Asp 340 345 350	1056
ACC CAC CCA CCA GCT TCT CTG AGG CTT CTG CCC CAG GTG TCG GCC TGG Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp 355 360 365	1104
GCT GGG TTA AGG GGG ACC GGC CAG GTC GGG ATC AGC CCC TCC Ala Gly Leu Arg Gly Thr Gly Gln Val Gly Ile Ser Pro Ser 370 375 380	1146
TGAGTGGCCA GCCTTCCCC CTGTGAAAGC AAAATAGCTT GGACCCCTTC AAGTTGAGAA	1206
CTGGTCAGGG CAAACCTGCC TCCCATTCTA CTCAAAGTCA TCCCTCTGTT CACAGAGATG	1266
GATGCATGTT CTGATTGCC CTTGGAGAA GCTCATCAGA AACTAAAAG AAGGCCACTG	1326
TTTGTCTCAC CTACCCATGA CCTGAAGCCC CTCCCTGAGT GGTCCCCACC TTTCTGGACG	1386
GAACCACGTA CTTTTTACAT ACATTGATTG ATGTCTCACG TCTCCCTAAA AATCGCTAAC	1446
ACCAAGCTGT GCCCTGACCA CCCTGGGCCCTGTCAG GACCTCCTGA GGCTTTGGCA	1506

AATAAACCTC CTAAAATGAA AAAAAAAA AAA

1539

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Phe	Gly	Leu	Ala	Leu	Leu	Ala	Gly	Leu	Leu	Gly	Leu	Leu	
1				5				10				15			
Leu	Gly	Gln	Ser	Leu	Gln	Val	Lys	Pro	Leu	Gln	Val	Glu	Pro	Pro	Glu
				20			25				30				
Pro	Val	Val	Ala	Val	Ala	Leu	Gly	Ala	Ser	Arg	Gln	Leu	Thr	Cys	Arg
	35					40				45					
Leu	Ala	Cys	Ala	Asp	Arg	Gly	Ala	Ser	Val	Gln	Trp	Arg	Gly	Leu	Asp
	50					55				60					
Thr	Ser	Leu	Gly	Ala	Val	Gln	Ser	Asp	Thr	Gly	Arg	Ser	Val	Leu	Thr
	65				70				75				80		
Val	Arg	Asn	Ala	Ser	Leu	Ser	Ala	Ala	Gly	Thr	Arg	Val	Cys	Val	Gly
		85					90				95				
Ser	Cys	Gly	Gly	Arg	Thr	Phe	Gln	His	Thr	Val	Gln	Leu	Leu	Val	Tyr
		100				105					110				
Ala	Phe	Pro	Asp	Gln	Leu	Thr	Val	Ser	Pro	Ala	Ala	Leu	Val	Pro	Gly
	115				120				125						
Asp	Pro	Glu	Val	Ala	Cys	Thr	Ala	His	Lys	Val	Thr	Pro	Val	Asp	Pro
	130				135				140						
Asn	Ala	Leu	Ser	Phe	Ser	Leu	Leu	Gly	Gly	Gln	Glu	Leu	Glu	Gly	
	145					150				155			160		
Ala	Gln	Ala	Leu	Gly	Pro	Glu	Val	Gln	Glu	Glu	Glu	Pro	Gln		
		165				170				175					
Gly	Asp	Glu	Asp	Val	Leu	Phe	Arg	Val	Thr	Glu	Arg	Trp	Arg	Leu	Pro
		180				185				190					
Pro	Leu	Gly	Thr	Pro	Val	Pro	Pro	Ala	Leu	Tyr	Cys	Gln	Ala	Thr	Met
	195				200					205					
Arg	Leu	Pro	Gly	Leu	Glu	Leu	Ser	His	Arg	Gln	Ala	Ile	Pro	Val	Leu
	210				215					220					
His	Ser	Pro	Thr	Ser	Pro	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Ser
	225				230				235			240			

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Pro Asp Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Gln Glu Pro
245 250 255

Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro
260 265 270

Ala Pro Gln Gln Gly Ser Thr His Thr Pro Arg Ser Pro Gly Ser Thr
275 280 285

Arg Thr Arg Arg Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu
290 295 300

Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala
305 310 315 320

Ala Leu Trp Thr Ser Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu
325 330 335

Pro Thr Tyr His Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Asp
340 345 350

Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp
355 360 365

Ala Gly Leu Arg Gly Thr Gly Gln Val Gly Ile Ser Pro Ser
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGC ATG GAT CGG GGC CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC 48
Met Asp Arg Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu
1 5 10 15

CTC CAG CCG GGC TGC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG 96
Leu Gln Pro Gly Cys Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val
20 25 30

GAG CCC CCG GAG CCG GTG GTG GCC GTG GCC CTG GGC GCC TCT CGC CAG
Glu Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln
35 40 45 144

CTC ACC TGC CGC CTG GAC TGC GCG GAC CGC GGG GCC ACG GTG CAG TGG Leu Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp 50 55 60	192
CGG GGC CTG GAC ACC AGC CTG GGC GCG GTG CAG TCG GAC GCG GGC CGC Arg Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg 65 70 75	240
AGC GTC CTC ACC GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGT Ser Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg 80 85 90 95	288
GTG TGC GTG GGC TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CGG Val Cys Val Gly Ser Cys Gly Arg Thr Phe Gln His Thr Val Arg 100 105 110	336
CTC CTT GTG TAC GCC TTC CCG GAC CAG CTG ACC ATC TCC CCG GCA GCC Leu Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala 115 120 125	384
CTG GTG CCT GGT GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG Leu Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr 130 135 140	432
CCT GTG GAC CCC AAT GCG CTC TCC TTC TCC CTG CTC CTG GGG GAC CAG Pro Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Leu Gly Asp Gln 145 150 155	480
GAA CTG GAG GGG GCC CAG GCT CTG GGC CCG GAG GTG GAG GAG GAG GAG Glu Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu 160 165 170 175	528
GAG GAG CCC CAG GAG GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC Glu Glu Pro Gln Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg 180 185 190	576
TGG CGG CTG CCG ACC CTG GCA ACC CCT GTC CTG CCC GCG CTC TAC TGC Trp Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys 195 200 205	624
CAG GCC ACG ATG AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC Gln Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala 210 215 220	672
ATC CCG GTC CTG CAC GGC CCG ACC TCC CGG GAG CCC CCC GAC ACG ACC Ile Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr 225 230 235	720
TCC CCG GAA CCC CGG GCC GCG ACC TCC CCG GAG ACC ACC CCC CAG CAG Ser Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln 240 245 250 255	768
GGC TCC ACA CAC AGC CCC AGG AGC CCG GGC TCT ACC AGG ACT TGC CGC Gly Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg 260 265 270	816
CCT GAG ATC TCC CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr 275 280 285	864

GGC TCG TCC AAA CCT ACG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC Gly Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr 290 295 300	912
AGC AGT GCG GTG CTG GGA CTG CTG CTC CTG GCT TTG CCC ACC TAC CAC Ser Ser Ala Val Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His 305 310 315	960
CTC TGG AAA CGT TGC CGG CAC CTG GCT GAG GAC GGC GCC CAC CCA CCA Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro 320 325 330 335	1008
GCT TCT CTG AGT AGC CAG CCC TTC CCC CTG TGAAGGGAAA ATAGGTTGGA Ala Ser Leu Ser Gln Pro Phe Pro Leu 340 345	1058
CCCCTTCAAG CTGAGAACTG GTCGGGGCAA ACCTGCCTCC CATTCTATTC AAAGTCATCG CTCTGGTCAC AGAGAGGGAC GCACATTCTG ATTGCCTCCT TTGGAAAGGC TCATCAGAAA CTCAAAAGAA GGTGATCGTT TGTCCCGCCT ACCCGTGACC TGGAAGCCCC CGCCCCGCTC GAGTGACCCC TGACTTTCTG GACGGAACCA ACGTACTTCT TACATATATT GATTGATGTG TCATATCTCC CTAAAATGCG TAAAACCAGC TGTGCCCGA CCACCTTGGG CCCCTGCCAT CAGGACCTCC TGAGGCTTTG GCAAATAAAC CTCCTAAAAG GATAGAAACT GAAACTTGTG GCCGGGCGCG GTGGCTCAAG CCTGTAATCC CAGCACTTTG GGAGGCCGAG GTGGGTGGAT CACGAGGTCA GGAGATCGAG ACCATCCTGG CTAACCCGTG AAACCCGTC TCTACTAAAA AAATACAAAA ATTAGCCGGG AGCGGTGGCG GGCGCCTGTA GTCCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCGTG AACCCGGGAG GCGGAGCTG CAGTGAGCTG AGATCCGGCC ACTGCACTCC AGCCTGGGG ACAGAGCGAG ACTCCGTCTC AAAAAAAA AAAAAAAA AAA	1118 1178 1238 1298 1358 1418 1478 1538 1598 1658 1718 1721

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Arg Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu 1 5 10 15
--

Gln Pro Gly Cys Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu 20 25 30

Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu
 35 40 45

Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp Arg
 50 55 60

Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg Ser
 65 70 75 80

Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val
 85 90 95

Cys Val Gly Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Arg Leu
 100 105 110

Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala Leu
 115 120 125

Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro
 130 135 140

Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Leu Gly Asp Gln Glu
 145 150 155 160

Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu
 165 170 175

Glu Pro Gln Glu Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp
 180 185 190

Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys Gln
 195 200 205

Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile
 210 215 220

Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr Ser
 225 230 235 240

Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln Gly
 245 250 255

Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg Pro
 260 265 270

Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly
 275 280 285

Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser
 290 295 300

Ser Ala Val Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu
 305 310 315 320

Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro Ala
 325 330 335

Ser Leu Ser Ser Gln Pro Phe Pro Leu
 340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCTACTGCC AGGCCACG

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCCTGGGAG ATCTCAGGG

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCACGATGA GGCTGCCTGG

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGGAGCCTG GGCTCCTGGG

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAGCTTCC ACCATGGATT TCGGACTGGC CC

32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGACTAGTG TCGGGCTGTG CAGGAC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGACTAGTGG TTTGGACGAG CCTGTTG

27

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Leu Asp Thr Ser Leu

1

5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"

/label= variable
/note= "Xaa = Ile or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"

/label= variable
/note= "Xaa = Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"

/label= variable
/note= "Xaa = Thr or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"

/label= variable
/note= "Xaa = Pro or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Xaa Xaa Xaa Xaa Leu
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Ile Asp Ser Pro Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Asp Thr Ser Leu
1 5